

-continued

445	450	455	460	
ACA GAT GAT GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA				8054
Thr Asp Asp Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser	465	470	475	
ATG AAG AAG ATG AGT ATG AAG ATC AAG CCC TTC TTC CCA CAG CAA TAGTCCCC				8109
Met Arg Lys Met Ser Met Lys Ile Arg Pro Phe Phe Pro Gln Gln	480	485	490	
TACGTAGATT TTTGCTCTTC TGTATGTGAC AACATTTTTT TACATTATGT TATTGGAATT				8169
TTCTTTCATA CATTATATTC CTCTAAAAC TCAAGCAGA CGTGAGTGTG ACTTTTTGAA				8229
AAAAAGTATAG GATAAATTAC ATTAAAAATAG CACATGATTT TCTTTTGTTT TCTTCATTTT				8289
TCTTGCTCAC CCAAGAAAGTA ACAAAGTAT AGTTTTGACA GAGTTGGTGT TCATAATTTT				8349
AGTTCTAGTT GATTGCGAGA ATTTTCAAAT AAGGAAGAGG GGTCTTTTAT CCTTGTGTA				8409
GGAAAAACCAT GACGGAAAGG AAAAACTGAT GTTTAAAAAGT CCACTTTTAA AACTATATTT				8469
ATTTATGTAG GATCTGTCAA AGAAAACTTC CAAAAAGATT TATTAATTAA ACCAGACTCT				8529
GTTCGAATAA GTTAATGTTT TCTTGTTTTG TAATCCACAC ATTCAATGAG TTAGGCTTTG				8589
CACTTGTAAAG GAAGGAGAAAG CTTTCACAAC CTCAAATAGC TAATAAACCG GTCTTGAATA				8649
TTTGAAGATT TAAAATCTGA CTCTAGGACG GGCACGGTGG CTCACGACTA TAATCCCAAC				8709
ACTTTGGGAG GCTGAGGCGG GCGGTCACAA GGTCAAGGAGT TCAAGACCA GCTGACCAAT				8769
ATGGTGAAAC CCCATCTCTA CTAAAAATAC AAAAAATTAGC CAGGCGTGGT GGCAGGTGCC				8829
TGTAGGTCCC AGCTAGCCTG TGAGGTGGAG ATTGCATTGA GCCAAGATC				8878

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SBQ ID NO:4:

Met	Lys	Arg	Met	Val	Ser	Trp	Ser	Phe	His	Lys	Leu	Lys	Thr	Met	Lys	
1				5					10					15		
His	Leu	Leu	Leu	Leu	Leu	Leu	Cys	Val	Phe	Leu	Val	Lys	Ser	Gln	Gly	
			20				25						30			
Val	Asn	Asp	Asn	Glu	Glu	Gly	Phe	Phe	Ser	Ala	Arg	Gly	His	Arg	Pro	
		35					40					45				
Leu	Asp	Lys	Lys	Arg	Glu	Glu	Ala	Pro	Ser	Leu	Arg	Pro	Ala	Pro	Pro	
	50				55						60					
Pro	Ile	Ser	Gly	Gly	Gly	Tyr	Arg	Ala	Arg	Pro	Ala	Lys	Ala	Ala	Ala	
65				70					75					80		
Thr	Gln	Lys	Lys	Val	Glu	Arg	Lys	Ala	Pro	Asp	Ala	Gly	Gly	Cys	Leu	
			85					90						95		
His	Ala	Asp	Pro	Asp	Leu	Gly	Val	Leu	Cys	Pro	Thr	Gly	Cys	Gln	Leu	
		100					105						110			
Gln	Glu	Ala	Leu	Leu	Gln	Gln	Glu	Arg	Pro	Ile	Arg	Asn	Ser	Val	Asp	
		115				120						125				
Gln	Leu	Asn	Asn	Asn	Val	Glu	Ala	Val	Ser	Gln	Thr	Ser	Ser	Ser	Ser	
	130				135						140					
Phe	Gln	Tyr	Met	Tyr	Leu	Leu	Lys	Asp	Leu	Trp	Gln	Lys	Arg	Gln	Lys	
145				150					155					160		
Gln	Val	Lys	Asp	Asn	Glu	Asn	Val	Val	Asn	Glu	Tyr	Ser	Ser	Glu	Leu	
			165					170						175		